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(51) International Patent Classification ⁶ : C12N 15/00, C07K 14/47, C12N 15/12, 15/10	A2	(11) International Publication Number: WO 98/03643 (43) International Publication Date: 29 January 1998 (29.01.98)
(21) International Application Number: PCT/EP97/03960 (22) International Filing Date: 17 July 1997 (17.07.97) (30) Priority Data: 9615351.5 22 July 1996 (22.07.96) GB 9618804.0 9 September 1996 (09.09.96) GB 9709239.9 8 May 1997 (08.05.97) GB (71) Applicants (for all designated States except US): SMITHKLINE BEECHAM PHARMA GMBH [DE/DE]; Leopoldstrasse 175, D-80804 Munich (DE). SMITHKLINE BEECHAM AUSTRALIA PTY. LTD. [AU/AU]; 300 Frankston Road, Dandenong, VIC 3175 (AU). (72) Inventors; and (75) Inventors/Applicants (for US only): LICHTENTHALER, Stefan [DE/DE]; University of Heidelberg, Im Neuenheimer Feld 282, D-69120 Heidelberg (DE). PRIOR, Peter [DE/DE]; University of Heidelberg, Im Neuenheimer Feld 282, D-69120 Heidelberg (DE). MASTERS, Colin, Louis [AU/AU]; Walter Boas Building, The University of Melbourne, Parkville, VIC 3052 (AU). BEYREUTHER, Konrad [DE/DE]; University of Heidelberg, Im Neuenheimer Feld 282, D-69120 Heidelberg (DE).	(74) Agent: VALENTINE, Jill; SmithKline Beecham, Corporate Intellectual Property, Two New Horizons Court, Brentford, Middlesex TW8 9EP (GB). (81) Designated States: JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>Without international search report and to be republished upon receipt of that report.</i>	
(54) Title: TRANSGENIC ANIMALS WITH MUTANT HUMAN APP OR A4CT SEQUENCES (57) Abstract Constructs comprising a human APP or A4CT DNA sequence encoding mutations which lead to a higher ratio of $\beta A_{41-42}/\beta A_{41-40}$ than wild type and their use in the production of transgenic animals developing amyloid plaques as a model of Alzheimer's disease.		

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TRANSGENIC ANIMALS WITH MUTANT HUMAN APP OR A4CT SEQUENCES

This invention relates to modified amyloid precursor proteins and their use in the production of transgenic animals.

The main protein component of the amyloid plaques found in the brain of
5 Alzheimer's disease (AD) patients is β A4, a 4 kDa peptide consisting of mainly forty and
forty-two residues (β A4₁₋₄₀, β A4₁₋₄₂) being derived from the amyloid precursor protein
(APP). By an enzyme called β -secretase APP can be cleaved at the N-terminus of β A4
generating a soluble APP and the C-terminal fragment A4CT (C99). This 99 residue
long membrane protein A4CT (ref. 1) which is the direct precursor for β A4 contains the
10 entire β A4 domain, the membrane domain and the cytoplasmic tail of APP. Alternative
processing of APP in a post-Golgi-compartment by a protease termed α -secretase leads
to the cleavage of APP within the β A4 domain yielding secretory APP and the
transmembrane fragment p3CT which is the direct precursor for p3.

Both C-terminal fragments of APP, A4CT and p3CT, are cleaved within the
15 membrane domain by a γ -cleavage activity, thereby releasing β A4 and p3 into the
medium (refs. 2, 3). In cells expressing wild type APP the site of γ -cleavage is mainly
the peptide bond Val(40)-Ile(41) of A4CT and to a minor extent the bond Ala(42)-
Thr(43). In cells expressing APP with the Familial AD linked mutations at Val 717
(based on APP770, Val 46 of A4CT) an increased γ -cleavage occurs behind Val(42), thus
20 producing larger amounts of β A4₁₋₄₂ (ref. 4).

Transgenic mice expressing A4CT have been produced using the human APP
promoter (ref. 5), the human thy-1 promoter (ref. 6) and the JC viral early region
promoter (ref. 7). Numerous promoters have been used in conjunction with the full
length APP cDNA (ref. 12). Generation of transgenic mammals bearing APP derived
25 DNA sequences are also described in WO93/14200 (TSI Corporation), WO91/19810
(California Biotechnology Inc), WO93/02189 (University of California), WO89/00689,
WO92/06187 (The Upjohn Company), EP0451700 (Miles Inc.), WO92/13069 (Imperial
College of Science Technology and Medicine) and WO89/06689 (McClellan Hospital
Corporation).

30 Results obtained depend upon the source of the promoter and the protein coding
sequence used. However in all cases described to date the nature of the APP-
immunoreactive deposits did not resemble the clinical situation and, with the exception
of the model described in reference 13 such transgenic animals have not been found to be
faithful model systems for Alzheimer's disease.

35 The β A4₁₋₄₂ peptide is the major subunit of amorphous and neuritic plaques in
Alzheimer's disease.

Applicants have found that recombinant cells expressing A4CT carrying certain mutations in the A4CT amino acid sequence lead to a higher ratio of $\beta A4_{1-42}/\beta A4_{1-40}$ than wild type and such mutant proteins and coding DNA are therefore useful in the production of transgenic animals developing amyloid plaques as a model of Alzheimer's disease. It will be understood that references herein to A4CT, $\beta A4_{1-42}$ and $\beta A4_{1-40}$ include all N-terminal variants produced by alternative cleavage during processing.

According to the present invention there is provided a non-human transgenic mammal whose cells contain a construct comprising a human APP or A4CT DNA sequence encoding a mutation selected from:

- 10 (i) T43A, T43S, T43G, T43V, T43L, T43I or T43F; and
 - (ii) Insertion in the transmembrane domain (residues 43 to 52) of a sequence of 1 to 10 amino acid residues;
- (numbering relative to A4CT) operably linked to a promoter sequence.

In a preferred aspect the construct encodes mutations (i) and (ii).

- 15 Mutation (i) is preferably selected from T43A and T43S.

Insertion (ii) is preferably located between residues 42 and 53, more preferably between 46 and 53. In a preferred embodiment the insertion is located between T48 and L49. The residues for insertion (ii) are preferably selected from F, I, G, Y, L, A, P, W, M, S, T, N and Q. The insertion (ii) is preferably 2 to 6 residues long. In a preferred embodiment the insertion (ii) is LV.

In a further preferred aspect the construct additionally encodes a mutation selected from:

V46F, V46I, V46G, V46Y, V46L, V46A, V46P, V46W, V46M, V46S, V46T, V46N or V46Q. In a preferred embodiment the additional mutation is V46F.

- 25 In a preferred embodiment the construct further encodes the APP signal sequence (APP residues 1 to 17) immediately upstream of the APP or A4CT DNA sequence. Hydrophobic residue inserts such as LeuGlu or Met are necessary for processing of A4CT to $\beta A4$ and should preferably be included between the signal peptide and A4CT coding regions and will remain attached to the processed A4CT.

- 30 The invention also relates to mammalian cells expressing the construct and to the DNA construct itself and vectors containing it.

Generation of transgenic mammals of the invention may be carried out conventionally, for example as described in WO93/14200, WO91/19810, WO93/02189, WO89/00689, WO92/06187, EP0451700, WO92/13069 and WO89/06689.

- 35 The APP or A4CT coding DNA is obtained by probing a human cDNA library. Mutations may be introduced by site-directed mutagenesis or during construction of the coding DNA from appropriate fragments.

Suitable promoters for use in the present invention include: Human APP (ref. 5); rat neuron specific enolase (neurons) (ref. 18); human β actin (ref. 19); human PDGF β (ref. 20); mouse Thy 1 (ref. 21); mouse Prion protein promoter (PrP) (ref. 14); rat synapsin 1 (brain) (ref. 22); human FMR1 (brain) (ref. 23); human neurofilament low (ref. 24), middle (brain) (ref. 25); NEX-1 (brain) (ref. 26); mouse APLP2 (brain) (ref. 27); rat alpha tubulin (ref. 28); mouse transferrin (ref. 29); mouse HMGCR (3-hydroxy-3-methylglutaryl coenzyme A reductase, oligodendrocytes) (ref. 30) and mouse myelin basic protein (ref. 31).

A tetracycline-inducible system may also be used, which has the advantage of regulating the gene expression (induction/repression) (refs. 33, 32). This system uses two constructs: a minimal promoter (PhCMV*-1) fused to seven tetracyclic operator sequences and the cDNA in question; and a transgene containing the tetracycline-controlled trans-activator protein (tTA) coding sequence under the control of a promoter, for example taken from the above list. Each construct is used to generate a transgenic mouse. Crossing the two homozygous mice generates a double transgenic line which expresses the tTA according to the chosen promoter. This tTA induces expression of the cDNA by activating the PhCMV*-1, but only in the absence of tetracycline. In the presence of tetracycline there is only basal expression.

A preferred promoter is the mouse Prion protein promoter (ref. 14)
The construct is prepared by conventional recombinant DNA techniques (ref. 10).
The transgenic mammal is produced by conventional techniques (refs. 8, 15, 16, 17).

In one aspect, the transgenic mammal is produced by introduction of the construct into an embryo, insertion of the embryo into a surrogate mother and allowing the embryo to develop to term.

The construct is prepared for transfer to the host animal by cleavage of vector containing the construct and purification of the DNA (ref. 8)

The transfer is carried out conventionally preferably using microinjection as described in detail in reference 8.

In an alternative aspect the transgenic mammal is produced by introduction of the construct into embryonic stem cells by conventional methods such as calcium phosphate/DNA precipitation, direct injection or electroporation (ref. 9) followed by injection of the transformed cells into blastocytes and insertion of the resulting embryo into a surrogate mother as described above.

Transgenic animals are identified by DNA analysis using Southern blot and PCR to detect founder animals.

The transgenic mammal is preferably a rodent such as rat or mouse, more preferably a mouse.

Mammalian cells expressing the construct may be prepared by conventional methods.

5 Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or
10 amplifying the human genes. The culture conditions, such as temperature, pH and the like will be apparent to the ordinarily skilled artisan.

Various mammalian cell culture systems can be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell, 23:175 (1981), and other cell lines
15 capable of expressing a compatible vector, for example, the SH-SY5Y, CHO and HeLa cell lines.

The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

Mammalian expression vectors will comprise an origin of replication, a suitable
20 promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

25 In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as hygromycin or neomycin resistance for eukaryotic cell culture.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction
30 endonuclease site(s) by procedures known in the art. Such procedures and others are deemed to be within the scope of those skilled in the art.

The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. Examples of such promoters include the CMV promoter, pCEP4 (Invitrogen) and other
35 promoters known to control expression of genes in eukaryotic cells or their viruses and replicable and viable in the host.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, lipofectin-mediated transfection, or electroporation. (Davis, L., Dibner, M., Battey, I., Basic Methods in Molecular Biology, (1986)).

- 5 The transgenic mammal or cells of the invention may be used to screen for drugs which inhibit deposit of β A4 by administering test drug to the mammal or cell culture medium and observing changes in APP expression and processing, histopathology and/or behavioural changes. The invention extends to such method of screening.

Suitable techniques for making such observations are described in WO93/14200.

10 Examples

The following constructs with sequences given in Table 2 were prepared by site directed mutagenesis of wtSPA4CT (ref.1):

- (1) SPA4CT T43S (SEQ ID NOs: 1 and 2)
- (2) SPA4CT T43A (SEQ ID NOs: 3 and 4)
- 15 (3) SPA4CT T43F (SEQ ID NOs: 5 and 6)
- (4) SPA4CT T43A+V46F (SEQ ID NOs: 7 and 8)
- (5) SPA4CT T43G+V46F (SEQ ID NOs: 9 and 10)
- (6) SPA4CT C-terminal insertion ('CTI') in the transmembrane domain (LV between T48 and L49) (SEQ ID NOs: 11 and 12)
- 20 as well as a construct carrying the FAD mutation SPA4CT V46F.

- wtSPA4CT consists of the 17 amino acid long signal peptide of APP followed by two additional amino acids of APP 695 (Leu and Glu) and then continuing with the β A4 sequence and the whole C-terminal domain and the mutagenesis was carried out in vector pSP65/SPA4CT (ref. 11). Additionally the mutagenesis leading to construct (3)
- 25 SPA4CT T43F was carried out in pBS/SPA4CT rev. pBS/SPA4CT rev was obtained by cloning the KpnI/Nhe fragment of pCEP/SPA4CT (ref. 2) in the pBS/SPC99 vector (ref. 34) that was digested with KpnI/XbaI.

The constructs were inserted into pCEP vector (ref. 2) and were stably transfected into COS7 cells.

30

Biological activity

Measurement of β A4 in the conditioned medium

- Stably transfected COS7 cells were metabolically labeled over night in methionine free MEM-medium containing 10% FCS and 133 μ Ci/ml 35 S-methionine.
- 35 β A4 and A4CT were immunoprecipitated, separated on a 10% Tris-Tricine gel and quantified by phosphorimaging. The following antibodies were used:

G2-10 (monoclonal) against synthetic peptide $\beta A4_{33-40}$ for the immunoprecipitation of $\beta A4_{n-40}$.

G2-11 (monoclonal) against synthetic peptide $\beta A4_{35-42}$ for the immunoprecipitation of $\beta A4_{n-42}$.

- 5 692 (polyclonal rabbit serum) against synthetic peptide $\beta A4_{1-40}$ for the immunoprecipitation of $\beta A4_{n-40}$ and $n-42$ stand for peptides with a defined C-terminus (ie residue 40 or 42 respectively of $\beta A4$) but allowing for possible N-terminal homogeneity. The full length $\beta A4$ forms produced by the particular constructs described herein contain Leu, Glu at positions -2, -1.

10

Detection of A4CT in the cell lysate

- The stably transfected COS7 cells were metabolically labeled for 10 min in methionine free MEM-medium containing 133 $\mu Ci/ml$ ^{35}S -methionine. In the cell lysate A4CT was immunoprecipitated with polyclonal antibody against A4CT (ref. 2),
 15 separated on a 10% Tris-Tricine gel and quantified by phosphorimaging.

Results

Expression of A4CT

- All constructs (wt SPA4CT and mutated SPA4CT) were expressed in similar
 20 amounts. The signal peptide of SPA4CT was completely removed leading to Leu-Glu-A4CT.

Release of $\beta A4$

- All A4CT constructs were processed to $\beta A4$ and produce similar amounts of
 25 $\beta A4$.

Generation of $\beta A4_{1-42}$ and $\beta A4_{1-40}$

- For all the constructs both $\beta A4$ species $\beta A4_{1-42}$ and $\beta A4_{1-40}$ were released. The ratio $\beta A4_{1-42}/\beta A4_{1-40}$ was determined and the results are shown in Table I.

30

Table 1

SPA4CT	$\beta A4_{1-42}/\beta A4_{1-40}$	increase of $\beta A4_{1-42}/\beta A4_{1-40}$ relative to wt SPA4CT by factor	significance p (student's t test)
wildtype	4.7 ± 1.3	1.0	
V46F	17.1 ± 4.8	3.6	< 0.001
(1) T43S	7.7 ± 1.2	1.6	0.01
(2) T43A	10.7 ± 2.3	2.2	<0.02
(3) T43F	9.5 ± 1.5	2.0	<0.001
(4) T43A+V46F	26.5 ± 3.6	5.6	< 0.001
(5) T43G+V46F	27.5 ± 4.7	5.8	<0.001
(6) CTI	19.6 ± 2.2	4.1	<0.001

Conclusions

5 The FAD linked mutation Val(717)Phe (Val(46)Phe of A4CT) is known to lead to a higher ratio of $\beta A4_{1-42}/\beta A4_{1-40}$ for both SPA4CT and APP compared with the wildtype proteins.

The above results demonstrate that SPA4CT expressing cells (COS7) generate the same $\beta A4$ species ($\beta A4_{1-40}$ and $\beta A4_{1-42}$) as APP expressing cells. This suggests that the
10 mechanism of $\beta A4$ generation is the same in APP and SPA4CT expressing cells.

The mutations near the C-terminus of $\beta A4$ are able to influence the γ -cleavage site, whereas the overall amount of generated $\beta A4$ as well as the ratio of $\beta A4/p3$ remain unchanged.

The single mutants (1), (2) and (3) have an increased ratio $\beta A4_{1-42}/\beta A4_{1-40}$ relative
15 to wt. The double mutants (4), (5) and (6) lead, respectively, to a 5.6-, 5.8 and 4.1-fold increase in $\beta A4_{1-42}/\beta A4_{1-40}$ relative to wt.

Generation of transgenic mice expressing SPA4CT T43A+V46F

The above described constructs which produce enhanced production of
20 $\beta A4_{1-42}$ relative to $\beta A4_{1-40}$ are useful for the generation of transgenic mice developing

amyloid plaques. By way of example, the construct SPA4CT T43A+V46F driven by the mouse Prion protein promoter (ref. 14) is used to transform a mouse by the following procedures:

The construct is prepared and purified.

- 5 Female mice are induced to superovulate and embryos are recovered.
DNA is microinjected into the pronucleus of embryos.
Embryos are transferred into pseudopregnant mice (female mice previously paired with vasectomised males).
Embryos are developed and mice are born.
- 10 Founder mice are identified by Southern blot and PCR and bred on.

Suitable mice lines are as follows:

Donor mice (embryos for pronucleus injection): B6D2F2

Acceptor mice: NMRI

- 15 Mice for further breeding: C57BL6

Screening of drugs using transgenic mice

The transgenic mice described above may be used to screen for potential activity of test drugs in the treatment of Alzheimer's disease.

- 20 APP expression and processing may be examined using detection of mRNA by Northern blots and detection of polypeptides using polyclonal and monoclonal antibodies that are specific to the terminal regions of the target peptides.

Histopathological observations may be made using immunohistological techniques to permit identification of amyloid plaques and in situ hybridisation using

- 25 labelled probes to target mRNA.

Observation of behavioural changes may employ conventional tests used to assess learning and memory deficits.

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Table 2: Sequence listings

(1) T43S

- 5 Protein
SEQ ID NO: 1
MLPGLALLLLAAWTARALED AEF RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA SVIVITLVMLK
KKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN
- 10 DNA
SEQ ID NO: 2
ATGCTGCCCCGGTTTGGCACTGCTCCTGCTGGCCGCCTGGACGGCTCGGGCGCTGGAGGATGCAGAATTCCGA
CATGACTCAGGATATGAAGTTCATCATCAAAAATTGGTGTCTTTGCAGAAGATGTGGGTTCAAACAAAGGT
GCAATCATTGGACTCATGGTGGGCGGTGTTGTTCATAGCTAGCGTGATCGTCATCACCTTGGTGATGCTTAAAG
15 AAGAAACAGTACACATCCATTCATCATGGTGTGGTGGAGGTTGACGCCGCTGTCACCCCAGAGGAGCGCCAC
CTGTCCAAGATGCAGCAGAACGGCTACGAAAATCCAACCTACAAGTTCTTTGAGCAGATGCAGAAC

(2) T43A

- 20 Protein
SEQ ID NO: 3
MLPGLALLLLAAWTARALED AEF RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA AVIVITLVMLK
KKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN
- 25 DNA
SEQ ID NO: 4
ATGCTGCCCCGGTTTGGCACTGCTCCTGCTGGCCGCCTGGACGGCTCGGGCGCTGGAGGATGCAGAATTCCGA
CATGACTCAGGATATGAAGTTCATCATCAAAAATTGGTGTCTTTGCAGAAGATGTGGGTTCAAACAAAGGT
GCAATCATTGGACTCATGGTGGGCGGTGTTGTTCATAGCGGCAGTGATCGTCATCACCTTGGTGATGCTTAAAG
30 AAGAAACAGTACACATCCATTCATCATGGTGTGGTGGAGGTTGACGCCGCTGTCACCCCAGAGGAGCGCCAC
CTGTCCAAGATGCAGCAGAACGGCTACGAAAATCCAACCTACAAGTTCTTTGAGCAGATGCAGAAC

(3) T43F

- 35 Protein
SEQ ID NO: 5
MLPGLALLLLAAWTARALED AEF RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA FVIVITLVMLK
KKQYTSIH HGVVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN
- 40 DNA
SEQ ID NO: 6
ATGCTGCCCCGGTTTGGCACTGCTCCTGCTGGCCGCCTGGACGGCTCGGGCGCTGGAGGATGCAGAATTCCGA
CATGACTCAGGATATGAAGTTCATCATCAAAAATTGGTGTCTTTGCAGAAGATGTGGGTTCAAACAAAGGT
GCAATCATTGGACTCATGGTGGGCGGTGTTGTTCATAGCATTCTGATCGTCATCACCTTGGTGATGCTGAAG
45 AAGAAACAGTACACATCCATTCATCATGGTGTGGTGGAGGTTGACGCCGCTGTCACCCCAGAGGAGCGCCAC
CTGTCCAAGATGCAGCAGAACGGCTACGAAAATCCAACCTACAAGTTCTTTGAGCAGATGCAGAAC

(4) T43A+V46F

- 50 Protein
SEQ ID NO: 7

MLPGLALLLLAAWTARALED AEF RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAAVIEITLVMLK
KKQYTSIHG VVEVDAAVTPEERHLSKMQQNGYENPTYKFFE QMQN

DNA

5 SEQ ID NO: 8

ATGCTGCCCGGTTTGGCACTGCTCCTGCTGGCCGCCTGGACGGCTCGGGCGCTGGAGGATGCAGAATTCCGA
CATGACTCAGGATATGAAGTTCATCATCAAAAATTGGTGTTCCTTGCAGAAGATGTGGGTTCAAACAAAGGT
GCAATCATTGGACTCATGGTGGGCGGTGTTGTCATAGCGGCAGTAATATTCATCACCTTGGTGATGCTTAAG
AAGAAACAGTACACATCCATTTCATCATGGTGTGGTGGAGGTTGACGCCGCTGTCACCCAGAGGAGCGCCAC
10 CTGTCCAAGATGCAGCAGAACGGCTACGAAAATCCAACCTACAAGTTCTTTGAGCAGATGCAGAAC

(5) T43G+V46F

Protein

15 SEQ ID NO: 9

MLPGLALLLLAAWTARALED AEF RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAGVIEITLVMLK
KKQYTSIHG VVEVDAAVTPEERHLSKMQQNGYENPTYKFFE QMQN

DNA

20 SEQ ID NO: 10

ATGCTGCCCGGTTTGGCACTGCTCCTGCTGGCCGCCTGGACGGCTCGGGCGCTGGAGGATGCAGAATTCCGA
CATGACTCAGGATATGAAGTTCATCATCAAAAATTGGTGTTCCTTGCAGAAGATGTGGGTTCAAACAAAGGT
GCAATCATTGGACTCATGGTGGGCGGTGTTGTCATAGCGGCGTAATATTCATCACCTTGGTGATGCTTAAG
AAGAAACAGTACACATCCATTTCATCATGGTGTGGTGGAGGTTGACGCCGCTGTCACCCAGAGGAGCGCCAC
25 CTGTCCAAGATGCAGCAGAACGGCTACGAAAATCCAACCTACAAGTTCTTTGAGCAGATGCAGAAC

(6) CTI

Protein

30 SEQ ID NO: 11

MLPGLALLLLAAWTARALED AEF RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVLM
LKKKQYTSIHG VVEVDAAVTPEERHLSKMQQNGYENPTYKFFE QMQN

DNA

35 SEQ ID NO: 12

ATGCTGCCCGGTTTGGCACTGCTCCTGCTGGCCGCCTGGACGGCTCGGGCGCTGGAGGATGCAGAATTCCGA
CATGACTCAGGATATGAAGTTCATCATCAAAAATTGGTGTTCCTTGCAGAAGATGTGGGTTCAAACAAAGGT
GCAATCATTGGACTCATGGTGGGCGGTGTTGTCATAGCGACAGTGATCGTCATCACCTTAGTACTCGTGATG
CTGAAGAAGAAACAGTACACATCCATTTCATCATGGTGTGGTGGAGGTTGACGCCGCTGTCACCCAGAGGAG
40 CGCCACCTGTCCAAGATGCAGCAGAACGGCTACGAAAATCCAACCTACAAGTTCTTTGAGCAGATGCAGAAC

Claims

1. A construct comprising a human APP or A4CT DNA sequence encoding a mutation selected from:
 - 5 (i) T43A, T43S, T43G, T43V, T43L, T43I or T43F; and
 - (ii) Insertion in the transmembrane domain (residues 43 to 52) of a sequence of 1 to 10 amino acid residues; (numbering relative to A4CT) operably linked to a promoter sequence.
2. A construct according to claim 1 wherein the construct encodes mutations (i) and
 10 (ii).
3. A construct according to claim 1 or 2 wherein mutation (i) is selected from T43A and T43S.
4. A construct according to any preceding claim wherein insertion (ii) is located between T48 and L49.
- 15 5. A construct according to any preceding claim wherein the residues for insertion (ii) are selected from F, I, G, Y, L, A, P, W, M, S, T, N and Q.
6. A construct according to any preceding claim wherein the insertion (ii) is 2 to 6 residues long.
7. A construct according to claim 6 wherein the insertion (ii) is LV.
- 20 8. A construct according to any preceding claim wherein the construct additionally encodes a mutation selected from:

V46F, V46I, V46G, V46Y, V46L, V46A, V46P, V46W, V46M, V46S, V46T, V46N or V46Q.
9. A construct according to any preceding claim wherein the construct further
 25 encodes the APP signal sequence (APP residues 1 to 17) immediately upstream of the APP or A4CT DNA sequence together with hydrophobic residue inserts between the signal peptide and A4CT coding regions.
10. A construct according to claim 1 comprising a sequence selected from:
 - (1) SPA4CT T43S (SEQ ID NO: 2)
 - 30 (2) SPA4CT T43A (SEQ ID NO: 4)
 - (3) SPA4CT T43F (SEQ ID NO: 6)
 - (4) SPA4CT T43A+V46F (SEQ ID NO: 8)
 - (5) SPA4CT T43G+V46F (SEQ ID NO: 10)
 - (6) SPA4CT C-terminal insertion ('CTI') in the transmembrane domain (LV between T48
 35 and L49) (SEQ ID NO: 12)
11. A construct according to any preceding claim comprising a mammalian promoter selected from Human APP; rat neuron specific enolase (neurons); human β actin; human

PDGF β ; mouse Thy 1; mouse Prion protein promoter (PrP); rat synapsin 1 (brain); human FMR1 (brain); human neurofilament low, middle (brain); NEX-1 (brain); mouse APLP2 (brain); rat alpha tubulin; mouse transferrin; mouse HMGCR (3-hydroxy-3-methylglutaryl coenzyme A reductase, oligodendrocytes) and mouse myelin basic

5 protein.

12. A non-human transgenic mammal whose cells contain a construct according to any preceding claim.

13. A transgenic mammal according to claim 12 which is a rodent.

14. A mammalian host cell expressing the construct of any of claims 1 to 11.

10 15. A vector containing the construct of any of claims 1 to 11.

16. A method of screening for drugs which inhibit deposit of β A4 by administering test drug to the transgenic mammal of claim 12 or 13 or cell culture medium containing the mammalian host cell of claim 14 and observing changes in APP expression and processing, histopathology and/or behavioural changes.

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(51) International Patent Classification ⁶ : C12N 15/00, A01K 67/027, C07K 14/47, C12N 15/12, 5/10		A3	(11) International Publication Number: WO 98/03643
			(43) International Publication Date: 29 January 1998 (29.01.98)
(21) International Application Number: PCT/EP97/03960			(74) Agent: VALENTINE, Jill; SmithKline Beecham, Corporate Intellectual Property, Two New Horizons Court, Brentford, Middlesex TW8 9EP (GB).
(22) International Filing Date: 17 July 1997 (17.07.97)			
(30) Priority Data:			
9615351.5 22 July 1996 (22.07.96) GB 9618804.0 9 September 1996 (09.09.96) GB 9709239.9 8 May 1997 (08.05.97) GB			
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(72) Inventors; and			
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(88) Date of publication of the international search report: 30 April 1998 (30.04.98)			
(54) Title: TRANSGENIC ANIMALS WITH MUTANT HUMAN APP OR A4CT SEQUENCES			
(57) Abstract			
Constructs comprising a human APP or A4CT DNA sequence encoding mutations which lead to a higher ratio of $\beta A_{41-42}/\beta A_{41-40}$ than wild type and their use in the production of transgenic animals developing amyloid plaques as a model of Alzheimer's disease.			

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INTERNATIONAL SEARCH REPORT

International Application No.
PCT/EP 97/03960

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/00 A01K67/027 C07K14/47 C12N15/12 C12N5/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 A01K C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	LICHTENTHALER, S. ET AL.: "Mutations near the C-terminus of beta-A4 influence the gamma cleavage of A4CT (C99) in COS7 cells." NEUROBIOLOGY OF AGING, vol. 17, no. 4 sup, 19 July 1996, pages s130-s131, XP002056699 see abstract 524	1,3,9,10
Y	----- see abstract 524	8,9, 12-16
Y	WO 93 14200 A (TSI CORP) 22 July 1993 cited in the application see the whole document ----- -/-	8,9, 12-16

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Date of the actual completion of the international search

23 February 1998

Date of mailing of the international search report

06/03/1998

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
T	<p>LICHTENTHALER, S.F. ET AL.: "Mutations in the transmembrane domain of APP altering gamma-secretase specificity"</p> <p>BIOCHEMISTRY.,</p> <p>vol. 36, no. 49, 9 December 1997, EASTON, PA US,</p> <p>pages 15396-15403, XP002056700</p> <p>see the whole document</p> <p>-----</p>	1-10

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP 97/03960

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